

Sequence Listing

<110> Baker, Kevin
Botstein, David
Eaton, Dan
Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William

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35 40 45
Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
50 55 60
Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
65 70 75
Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
80 85 90
Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
95 100 105
Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
110 115 120
Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
125 130 135
Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
140 145 150
Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
155 160 165
Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
170 175 180
Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
185 190 195
Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
200 205 210

Ile	Glu	Pro	Gly	Ala	Phe	Glu	Gly	Val	Thr	Val	Phe	His	Ile	Arg	215	220	225
Ile	Ala	Glu	Ala	Lys	Leu	Thr	Ser	Val	Pro	Lys	Gly	Leu	Pro	Pro	230	235	240
Thr	Leu	Leu	Glu	Leu	His	Leu	Asp	Tyr	Asn	Lys	Ile	Ser	Thr	Val	245	250	255
Glu	Leu	Glu	Asp	Phe	Lys	Arg	Tyr	Lys	Glu	Leu	Gln	Arg	Leu	Gly	260	265	270
Leu	Gly	Asn	Asn	Lys	Ile	Thr	Asp	Ile	Glu	Asn	Gly	Ser	Leu	Ala	275	280	285
Asn	Ile	Pro	Arg	Val	Arg	Glu	Ile	His	Leu	Glu	Asn	Asn	Lys	Leu	290	295	300
Lys	Lys	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Leu	Lys	Tyr	Leu	Gln	Ile	305	310	315
Ile	Phe	Leu	His	Ser	Asn	Ser	Ile	Ala	Arg	Val	Gly	Val	Asn	Asp	320	325	330
Phe	Cys	Pro	Thr	Val	Pro	Lys	Met	Lys	Lys	Ser	Leu	Tyr	Ser	Ala	335	340	345
Ile	Ser	Leu	Phe	Asn	Asn	Pro	Val	Lys	Tyr	Trp	Glu	Met	Gln	Pro	350	355	360
Ala	Thr	Phe	Arg	Cys	Val	Leu	Ser	Arg	Met	Ser	Val	Gln	Leu	Gly	365	370	375
Asn Phe Gly Met																	

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 <212> DNA
 <213> Artificial Sequence

<220>
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35 40 45
Arg Gly Ala Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu
50 55 60
Asp Glu Thr Trp His Pro Asp Leu Gly Gln Pro Phe Gly Val Met
65 70 75

Arg Cys Val Leu Cys Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg
80 85 90

Thr Arg Gly Pro Gly Arg Val Ser Cys Lys Asn Ile Lys Pro Glu
95 100 105

Cys Pro Thr Pro Ala Cys Gly Gln Pro Arg Gln Leu Pro Gly His
110 115 120

Cys Cys Gln Thr Cys Pro Gln Glu Arg Ser Ser Ser Glu Arg Gln
125 130 135

Pro Ser Gly Leu Ser Phe Glu Tyr Pro Arg Asp Pro Glu His Arg
140 145 150

Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala Glu Glu Arg Ala Arg
155 160 165

Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu Thr Gly Pro Arg
170 175 180

Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu Arg Ser Ser
185 190 195

Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro Thr Arg
200 205 210

Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His Pro
215 220 225

Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala
230 235 240

Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His
245 250 255

Val Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly
260 265 270

Pro Leu Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala
275 280 285

Ile Leu Thr Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile
290 295 300

Thr Leu Leu Thr Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu
305 310 315

Leu Leu Phe Arg Gly Leu Leu Glu Pro Arg Ser Gly Gly Leu Thr
320 325 330

Gln Val Pro Leu Arg Leu Gln Ile Leu His Gln Gly Gln Leu Leu
335 340 345

Arg Glu Leu Gln Ala Asn Val Ser Ala Gln Glu Pro Gly Phe Ala
350 355 360

Glu Val Leu Pro Asn Leu Thr Val Gln Glu Met Asp Trp Leu Val

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Leu Arg Ile Ser Gly His Ile Ala Ala Arg Lys Ser Cys Asp Val		
395	400	405
Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu Ile Pro Val Gln		
410	415	420
Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu Gly Asn Gly		
425	430	435
Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser Glu Val		
440	445	450
Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln Arg		
455	460	465
Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr		
470	475	480
Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met		
485	490	495
Leu Leu Gln Asn Glu Leu Phe Leu Asn Val Gly Thr Lys Asp Phe		
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Pro Asp Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys		
515	520	525
Gly His Ser Ala Arg His Asp Thr Leu Pro Val Pro Leu Ala Gly		
530	535	540
Ala Leu Val Leu Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala		
545	550	555
Trp Leu Ser Leu Asp Thr His Cys His Leu His Tyr Glu Val Leu		
560	565	570
Leu Ala Gly Leu Gly Gly Ser Glu Gln Gly Thr Val Thr Ala His		
575	580	585
Leu Leu Gly Pro Pro Gly Thr Pro Gly Pro Arg Arg Leu Leu Lys		
590	595	600
Gly Phe Tyr Gly Ser Glu Ala Gln Gly Val Val Lys Asp Leu Glu		
605	610	615
Pro Glu Leu Leu Arg His Leu Ala Lys Gly Met Ala Ser Leu Met		
620	625	630
Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu Leu Arg Gly Gln Val		
635	640	645
His Ile Ala Asn Gln Cys Glu Val Gly Gly Leu Arg Leu Glu Ala		
650	655	660

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Ala Gly Ala Glu Gly Val Arg Ala Leu Gly Ala Pro Asp Thr Ala	665	670	675
Ser Ala Ala Pro Pro Val Val Pro Gly Leu Pro Ala Leu Ala Pro	680	685	690
Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys	695	700	705
Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro	710	715	720
Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr	725	730	735
Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His	740	745	750
Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys	755	760	765
Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro	770	775	780
Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala	785	790	795
Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys	800	805	810
Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys	815	820	825
Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg	830	835	840
Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly	845	850	855
Ala His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg	860	865	870
Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp	875	880	885
His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys	890	895	900
Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser	905	910	915
Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser	920	925	930
Arg Cys Thr Ala His Arg Arg Pro Pro Glu Thr Arg Thr Asp Pro	935	940	945
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 <212> DNA
 <213> Artificial Sequence

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 <210> 10
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 <400> 12
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<400> 13
gcagggtgct caaacaggac ac 22

<210> 14
<211> 3231
<212> DNA
<213> Homo Sapien

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 <211> 737
 <212> PRT
 <213> Homo Sapien

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 20 25 30
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 35 40 45
 Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
 50 55 60
 Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
 65 70 75
 Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
 80 85 90
 Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
 95 100 105
 Gly Asn Cys Ser Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

09944862 083101

110	115	120
Cys Ile Cys Asn Glu Gly Tyr Glu Gly	Pro Asn Cys Glu Gln Ala	
125	130	135
Leu Pro Ser Leu Pro Ala Thr Gly Trp	Thr Glu Ser Met Ala Pro	
140	145	150
Arg Gln Leu Gln Pro Val Pro Ala Thr	Gln Glu Pro Asp Lys Ile	
155	160	165
Leu Pro Arg Ser Gln Ala Thr Val Thr	Leu Pro Thr Trp Gln Pro	
170	175	180
Lys Thr Gly Gln Lys Val Val Glu Met	Lys Trp Asp Gln Val Glu	
185	190	195
Val Ile Pro Asp Ile Ala Cys Gly Asn	Ala Ser Ser Asn Ser Ser	
200	205	210
Ala Gly Gly Arg Leu Val Ser Phe Glu	Val Pro Gln Asn Thr Ser	
215	220	225
Val Lys Ile Arg Gln Asp Ala Thr Ala	Ser Leu Ile Leu Leu Trp	
230	235	240
Lys Val Thr Ala Thr Gly Phe Gln Gln	Cys Ser Leu Ile Asp Gly	
245	250	255
Arg Ser Val Thr Pro Leu Gln Ala Ser	Gly Gly Leu Val Leu Leu	
260	265	270
Glu Glu Met Leu Ala Leu Gly Asn Asn	His Phe Ile Gly Phe Val	
275	280	285
Asn Asp Ser Val Thr Lys Ser Ile Val	Ala Leu Arg Leu Thr Leu	
290	295	300
Val Val Lys Val Ser Thr Cys Val Pro	Gly Glu Ser His Ala Asn	
305	310	315
Asp Leu Glu Cys Ser Gly Lys Gly Lys	Cys Thr Thr Lys Pro Ser	
320	325	330
Glu Ala Thr Phe Ser Cys Thr Cys Glu	Glu Gln Tyr Val Gly Thr	
335	340	345
Phe Cys Glu Glu Tyr Asp Ala Cys Gln	Arg Lys Pro Cys Gln Asn	
350	355	360
Asn Ala Ser Cys Ile Asp Ala Asn Glu	Lys Gln Asp Gly Ser Asn	
365	370	375
Phe Thr Cys Val Cys Leu Pro Gly Tyr	Thr Gly Glu Leu Cys Gln	
380	385	390
Ser Lys Ile Asp Tyr Cys Ile Leu Asp	Pro Cys Arg Asn Gly Ala	
395	400	405

Thr Cys Ile Ser Ser Leu Ser Gly Phe Thr Cys Gln Cys Pro Glu	410	415	420
Gly Tyr Phe Gly Ser Ala Cys Glu Glu Lys Val Asp Pro Cys Ala	425	430	435
Ser Ser Pro Cys Gln Asn Asn Gly Thr Cys Tyr Val Asp Gly Val	440	445	450
His Phe Thr Cys Asn Cys Ser Pro Gly Phe Thr Gly Pro Thr Cys	455	460	465
Ala Gln Leu Ile Asp Phe Cys Ala Leu Ser Pro Cys Ala His Gly	470	475	480
Thr Cys Arg Ser Val Gly Thr Ser Tyr Lys Cys Leu Cys Asp Pro	485	490	495
Gly Tyr His Gly Leu Tyr Cys Glu Glu Glu Tyr Asn Glu Cys Leu	500	505	510
Ser Ala Pro Cys Leu Asn Ala Ala Thr Cys Arg Asp Leu Val Asn	515	520	525
Gly Tyr Glu Cys Val Cys Leu Ala Glu Tyr Lys Gly Thr His Cys	530	535	540
Glu Leu Tyr Lys Asp Pro Cys Ala Asn Val Ser Cys Leu Asn Gly	545	550	555
Ala Thr Cys Asp Ser Asp Gly Leu Asn Gly Thr Cys Ile Cys Ala	560	565	570
Pro Gly Phe Thr Gly Glu Glu Cys Asp Ile Asp Ile Asn Glu Cys	575	580	585
Asp Ser Asn Pro Cys His His Gly Gly Ser Cys Leu Asp Gln Pro	590	595	600
Asn Gly Tyr Asn Cys His Cys Pro His Gly Trp Val Gly Ala Asn	605	610	615
Cys Glu Ile His Leu Gln Trp Lys Ser Gly His Met Ala Glu Ser	620	625	630
Leu Thr Asn Met Pro Arg His Ser Leu Tyr Ile Ile Ile Gly Ala	635	640	645
Leu Cys Val Ala Phe Ile Leu Met Leu Ile Ile Leu Ile Val Gly	650	655	660
Ile Cys Arg Ile Ser Arg Ile Glu Tyr Gln Gly Ser Ser Arg Pro	665	670	675
Ala Tyr Glu Glu Phe Tyr Asn Cys Arg Ser Ile Asp Ser Glu Phe	680	685	690
Ser Asn Ala Ile Ala Ser Ile Arg His Ala Arg Phe Gly Lys Lys			

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
725 730 735

Asp Leu

<210> 16

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 16

tgtaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 17

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 18

<211> 508

<212> DNA

<213> Homo Sapien

<400> 18

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acgaaagtgt gacccccctt tcaggettcc agggggactg gtcctcctgg 100

aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggatgaagg 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttcctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttcctgggta tactggagag 450

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taggggag 508

<210> 19

<211> 508

<212> DNA

<213> Homo Sapien

<400> 19

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acgaaagtgt gacccccctt tcaggctttc agggggactg gtcctcctgg 100

aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggatgaagg 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttctgggtta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 20

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 20

ctctggaagg tcacggccac agg 23

<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 21

ctcagttcgg ttggcaaagc tctc 24

<210> 22

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cagtgtctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

gctttgccaa ccgaactga 69

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

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gccacacca tgccgggcac ctacgtctcc tcgaccacac tcagtagtcc 150

cagcaccag ggctgcaag agcaggcacg ggccctgatg cgggacttcc 200

cgctcgtgga cggccacaac gacctgccc tggctctaag gcaggtttac 250

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<210> 24

<211> 433

<212> PRT

<213> Homo Sapien

<400> 24

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				20					25					30	
Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Leu	Val	Leu	Arg	Gln	
				35					40					45	
Val	Tyr	Gln	Lys	Gly	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	Ser	
				50					55					60	
Tyr	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly	
				65					70					75	
Ala	Gln	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg	
				80					85					90	
Asp	Ala	Leu	Arg	Leu	Thr	Leu	Glu	Gln	Ile	Asp	Leu	Ile	Arg	Arg	
				95					100					105	
Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	Lys	
				110					115					120	
Ala	Leu	Asn	Asp	Thr	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	Glu	
				125					130					135	
Gly	Gly	His	Ser	Leu	Asp	Asn	Ser	Leu	Ser	Ile	Leu	Arg	Thr	Phe	
				140					145					150	
Tyr	Met	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	His	Thr	Cys	Asn	
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Thr	Pro	Trp	Ala	Glu	Ser	Ser	Ala	Lys	Gly	Val	His	Ser	Phe	Tyr	
				170					175					180	

Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala	
				185					190					195	
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser	
				200					205					210	
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val	
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Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys	
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Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr	
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Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu	
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Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg	
				335					340					345	
Gln	Val	Glu	Lys	Val	Gln	Glu	Glu	Asn	Lys	Trp	Gln	Ser	Pro	Leu	
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Glu	Asp	Lys	Phe	Pro	Asp	Glu	Gln	Leu	Ser	Ser	Ser	Cys	His	Ser	
				365					370					375	
Asp	Leu	Ser	Arg	Leu	Arg	Gln	Arg	Gln	Ser	Leu	Thr	Ser	Gly	Gln	
				380					385					390	
Glu	Leu	Thr	Glu	Ile	Pro	Ile	His	Trp	Thr	Ala	Lys	Leu	Pro	Ala	
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Ala	Val	Val	Ala	Thr	Phe	Pro	Val	Leu	Ile	Leu	Trp	Leu			
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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25
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<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

cgtgatggtg tctttgtcca tggg 24

<210> 27

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

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<212> DNA

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<210> 29

<211> 1416

<212> DNA

<213> Homo Sapien

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gatccgcggc cggaattct aaaccaacat gccgggcacc tacgctccct 100

cgaccacact cagtagtccc agcaccagg gcctgcaaga gcaggcacgg 150

gccctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200

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<211> 446
<212> PRT
<213> Homo Sapien

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Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
20 25 30
Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45
Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

00944822 033401

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Tyr Gly Gln Thr	Ser Leu Asp Arg	Leu Arg Asp Gly	Leu Val Gly		
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Ala Gln Phe Trp	Ser Ala Tyr Val	Pro Cys Gln Thr	Gln Asp Arg		
	80		85		90
Asp Ala Leu Arg	Leu Thr Leu Glu Gln	Ile Asp Leu Ile	Arg Arg		
	95		100		105
Met Cys Ala Ser	Tyr Ser Glu Leu Glu	Leu Val Thr Ser	Ala Lys		
	110		115		120
Ala Leu Asn Asp	Thr Gln Lys Leu Ala	Cys Leu Ile Gly	Val Glu		
	125		130		135
Gly Gly His Ser	Leu Asp Asn Ser Leu	Ser Ile Leu Arg	Thr Phe		
	140		145		150
Tyr Met Leu Gly	Val Arg Tyr Leu Thr	Leu Thr His Thr	Cys Asn		
	155		160		165
Thr Pro Trp Ala	Glu Ser Ser Ala Lys	Gly Val His Ser	Phe Tyr		
	170		175		180
Asn Asn Ile Ser	Gly Leu Thr Asp Phe	Gly Glu Lys Val	Val Ala		
	185		190		195
Glu Met Asn Arg	Leu Gly Met Met Val	Asp Leu Ser His	Val Ser		
	200		205		210
Asp Ala Val Ala	Arg Arg Ala Leu Glu	Val Ser Gln Ala	Pro Val		
	215		220		225
Ile Phe Ser His	Ser Ala Ala Arg Gly	Val Cys Asn Ser	Ala Arg		
	230		235		240
Asn Val Pro Asp	Asp Ile Leu Gln Leu	Leu Lys Lys Asn	Gly Gly		
	245		250		255
Val Val Met Val	Ser Leu Ser Met Gly	Val Ile Gln Cys	Asn Pro		
	260		265		270
Ser Ala Asn Val	Ser Thr Val Ala Asp	His Phe Asp His	Ile Lys		
	275		280		285
Ala Val Ile Gly	Ser Lys Phe Ile Gly	Ile Gly Gly Asp	Tyr Asp		
	290		295		300
Gly Ala Gly Lys	Phe Pro Gln Gly Leu	Glu Asp Val Ser	Thr Tyr		
	305		310		315
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Gly Trp Ser	Glu Glu		
	320		325		330
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val	Phe Arg		
	335		340		345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu	350	355	360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser	365	370	375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln	380	385	390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala	395	400	405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His	410	415	420
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser	425	430	435
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	440	445	

<210> 31
 <211> 1790
 <212> DNA
 <213> Homo Sapien

<400> 31
 cgcccagcga cgtgcgggcg gectggcccg cgccctcccg cgcccggcct 50
 gcgtcccgcg ccctgcgcca ccgcccgcga gccgcagccc gccgcgcgcc 100
 ccgggcagcg ccggccccat gcccgcgggc cgccggggcc ccgcccacca 150
 atccgcgcgg cggccgcgcg cgttgctgcc cctgctgctg ctgctctgcg 200
 tcctcggggc gccgcgagcc ggatcaggag cccacacagc tgtgatcagt 250
 ccccaggatc ccacgcttct catcggtctc tcctgctgg ccacctgctc 300
 agtgcacgga gaccaccag gagccaccg cgagggcctc tactggacct 350
 tcaacgggcy cgccctgccc cctgagctct cccgtgtact caacgcctcc 400
 accttggtc tggccctggc caacctcaat ggggccaggc agcggctcgg 450
 ggacaacctc gtgtgocacg ccctgacgg cagcatcctg gctggctcct 500
 gcctctatgt tggcctgccc ccagagaaac ccgtcaacat cagctgctgg 550
 tccaagaaca tgaaggactt gacctgccgc tggacgccag gggcccacgg 600
 ggagaccttc ctccacacca actactccct caagtacaag cttaggtgg 650
 atggccagga caacacatgt gaggagtacc acacagtggg gcccactcc 700
 tgccacatcc ccaaggacct ggctctcttt acgccctatg agatctgggt 750
 ggaggccacc aaccgcctgg gctctgcccg ctccgatgta ctcacgctgg 800

atatacctgga tgtggtgacc acggaccccc cgcccagcgt gcacgtgagc 850
 cgcgctggggg gcctggagga ccagctgagc gtgcgctggg tgtcgccacc 900
 cgccctcaag gatttctctt ttcaagccaa ataccagatc cgctaccgag 950
 tggaggacag tgtggaactgg aaggtggtgg acgatgtgag caaccagacc 1000
 tcctgcccgc tggccggcct gaaacccggc accgtgtact tcgtgcaagt 1050
 gcgctgcaac ccctttggca tctatggctc caagaaagcc gggatctgga 1100
 gtgagtggag ccaccccaca gccgcctcca ctccccgcag tgagcgcccg 1150
 ggcccggggc gcggggcgctg cgaaccgcgg ggccggagagc cgagctcggg 1200
 gccggtgcgg cgcgagctca agcagttcct gggctggctc aagaagcacg 1250
 cgtactgctc caacctcagc ttccgcctct acgaccagtg gcgagcctgg 1300
 atgcagaagt cgcacaagac ccgcaaccag gacgagggga tcctgccctc 1350
 gggcagacgg ggcacggcga gaggtcctgc cagataagct gtaggggctc 1400
 aggccaccct ccctgccacg tggagacgca gaggccgaac ccaaactggg 1450
 gccacctctg taccctcact tcagggcacc tgagccaccc tcagcaggag 1500
 ctgggggtggc ccctgagctc caacggccat aacagctctg actcccacgt 1550
 gaggccacct ttgggtgcac cccagtgggt gtgtgtgtgt gtgtgaggg 1600
 tggttgagtt gcctagaacc cctgccaggg ctgggggtga gaaggggagt 1650
 cattactccc cattacctag gggccctcca aaagagtcct tttaaataaa 1700
 tgagctatctt aggtgctgtg attgtgaaaa aaaaaaaaaa aaaaaaaaaa 1750
 aaaaaaaaaa aaaaaaaaaa aaaaacaaaa aaaaaaaaaa 1790

<210> 32
 <211> 422
 <212> PRT
 <213> Homo Sapien

<400> 32
 Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg
 1 5 10 15
 Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu Cys Val Leu Gly
 20 25 30
 Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 35 40 45
 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
 50 55 60

009443552-0033101

Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr	65	70	75
Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val	80	85	90
Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly	95	100	105
Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp	110	115	120
Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro	125	130	135
Glu Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp	140	145	150
Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu	155	160	165
His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln	170	175	180
Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His Ser Cys	185	190	195
His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp	200	205	210
Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu	215	220	225
Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp	230	235	240
Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val	245	250	255
Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala	260	265	270
Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys	275	280	285
Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly	290	295	300
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro	305	310	315
Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp	320	325	330
Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly	335	340	345
Pro Gly Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser			

350	355	360
Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys		
365	370	375
Lys His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln		
380	385	390
Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp		
395	400	405
Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro		
410	415	420
Ala Arg		

<210> 33
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 33
 cccgcccgcac gtgcacgtga gcc 23

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 34
 tgagccagcc caggaactgc ttg 23

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 35
 caagtgcgct gcaacccctt tggcatctat gggtccaaga aagccgggat 50

<210> 36
 <211> 1771
 <212> DNA
 <213> Homo Sapien

<400> 36
 cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaagg 100
 atgaaatttc ttctggacat cctcctgctt ctcccgttac tgategtctg 150
 ctccctagag tccttcgtga agctttttat tcctaagagg agaaaatcag 200
 tcaccggcga aatcgtgctg attacaggag ctgggcatgg aattgggaga 250
 ctgactgctt atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
 tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350
 gtgccaaggt tcataccttt gtggtagact gcagcaaccg agaagatatt 400
 tacagctctg caaagaaggt gaaggcagaa attggagatg ttagtatttt 450
 agtaaataat gctgggtgtag tctatacatc agatttggtt gctacacaag 500
 atcctcagat tgaaaagact tttgaagtta atgtacttgc acatttctgg 550
 actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
 tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg 650
 cttactgttc aagcaagttt gctgctgttg gatttcataa aactttgaca 700
 gatgaactgg ctgccttaca aataactgga gtcaaaacaa catgtctgtg 750
 tcctaatttc gtaaacactg gcttcatcaa aaatccaagt acaagtttgg 800
 gaccactct ggaacctgag gaagtggtaa acaggctgat gcatgggatt 850
 ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
 aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa 950
 aaatcagtgt taagtttgat gcagttattg gatataaaat gaaagcgcaa 1000
 taagcaccta gttttctgaa aactgattta ccaggtttag gttgatgtca 1050
 tctaatagtg ccagaatttt aatgtttgaa cttctgtttt ttctaattat 1100
 cccattttct tcaatatcat ttttgaggct ttggcagtct tcatttacta 1150
 ccacttggtc tttagccaaa agctgattac atatgatata aacagagaaa 1200
 tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaatgac 1250
 tttattaaaa taatttccaa gattatttgt ggctcacctg aaggctttgc 1300
 aaaatttgta ccataaccgt ttatttaaca tatattttta tttttgattg 1350
 cacttaaatt ttgtataatt tgtgtttctt tttctgttct acataaaatc 1400
 agaaacttca agctctctaa ataaaatgaa ggactatata tagtggtatt 1450
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gccactctgt ttctgagag atacctcaca ttccaatgcc aaacatttct 1550
gcacagggaa gctagaggtg gatacacgtg ttgcaagtat aaaagcatca 1600
ctgggattta aggagaattg agagaatgta cccacaaatg gcagcaataa 1650
taaatggatc acacttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1750
aaaaaaaaaa aaaaaaaaaa a 1771

<210> 37
<211> 300
<212> PRT
<213> Homo Sapien

<400> 37
Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile
1 5 10 15
Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg
20 25 30
Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
35 40 45
His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys
50 55 60
Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu
65 70 75
Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe
80 85 90
Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys
95 100 105
Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn
110 115 120
Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro
125 130 135
Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp
140 145 150
Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly
155 160 165
His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro
170 175 180
Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
185 190 195
His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile Thr Gly

200	205	210
Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe		
215	220	225
Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu		
230	235	240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys		
245	250	255
Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu		
260	265	270
Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile		
275	280	285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln		
290	295	300

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 38

ggtgaaggca gaaattggag atg 23

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 39

atcccatgca tcagcctggt tacc 24

<210> 40

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 41

<211> 1377

<212> DNA

<213> Homo Sapien

<400> 41

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gaaccaggac tggggtgacg gcagggcagg gggcgcttg ccggggagaa 100
gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150
ccgaaggagg ccatcgggga gccgggaggg gggactgca gaggaccccg 200
gcgtccgggc tcccgtgcc agcgctatga ggccactcct cgtcctgctg 250
ctcctggggc tggcgcccg ctcgccccca ctggacgaca acaagatecc 300
cagcctctgc ccggggcacc ccggccttcc aggcacgccg ggccaccatg 350
gcagccaggg cttgccgggc cgcgatggcc gcgacggccg cgacggcgcg 400
cccggggctc cgggagagaa aggcgagggc gggaggcccg gactgccggg 450
acctcgaggg gaccccgggc cgcgaggaga ggccgggacc gcggggccca 500
ccgggcctgc cggggagtgc tcggtgcctc cgcgatccgc cttcagcgcc 550
aagcgctccg agagccgggt gcctccgccg tctgacgcac ccttgccctt 600
cgaccgcgtg ctggtgaacg agcagggaca ttacgacgcc gtcaccggca 650
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gtctaccggg ccagcctgca gtttgatctg gtgaagaatg gcgaatccat 750
tgccctcttc ttccagtttt tcgggggggtg gccaagcca gcctcgtct 800
cggggggggc catggtgagg ctggagcctg aggaccaagt gtgggtgcag 850
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gggccggccc ttttctcaga gatcactcaa taaacctaa aacctcata 1350
aaaaaaaaa aaaaaaaaaa aaaaaaa 1377

<210> 42

<211> 243
 <212> PRT
 <213> Homo Sapien

<400> 42

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Ser	Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro Gly
			20					25					30
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln Gly
			35					40					45
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro Gly
			50					55					60
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro Gly
			65					70					75
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala Gly
			80					85					90
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser Ala
			95					100					105
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser Asp
			110					115					120
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly His
			125					130					135
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly Val
			140					145					150
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu Gln
			155					160					165
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe Gln
			170					175					180
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly Ala
			185					190					195
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val Gly
			200					205					210
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp Ser
			215					220					225
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser Pro
			230					235					240
Val	Phe	Ala											

<210> 43
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 43
 tacaggccca gtcaggacca gggg 24

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 44
 agccagcctc gctctcgg 18

 <210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 45
 gtctgcatc aggtctgg 18

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 46
 gaaagaggca atggattcgc 20

 <210> 47
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 gacttacact tgccagcaca gcac 24

 <210> 48
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctcttttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50
atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100
acctgacggg cccaacagac ccatgctgca tccagagacc tccctgggcc 150
gggggcatct cctggctgtg ctctggccc tccttggcac caoctgggca 200
gaggtgtggc caccagct gcaggagcag gctccgatgg ccggagccct 250
gaacaggaag gagagtttct tgctcctctc cctgcacaac cgcttgcgca 300
gctgggtcca gccccctgcg gctgacatgc ggaggctgga ctggagtgc 350
agcctggccc aactggctca agccaggga gccctctgtg gaatcccaac 400
cccgagcctg gcatccggcc tgtggcgcac cctgcaagtg ggctggaaca 450
tgcagctgct gcccgcgggc ttggcgctct ttgttgaagt ggtcagccta 500
tggtttgcag aggggcagcg gtacagccac gcggcaggag agtgtgctcg 550
caacgccacc tgcaccact acacgcagct cgtgtgggcc acctcaagcc 600
agctgggctg tgggcggcac ctgtgctctg caggccagac agcgatagaa 650
gcctttgtct gtgcctactc ccccgaggc aactgggagg tcaacgggaa 700
gacaatcatc cctataaga agggcgctg gtgttcgctc tgcacagcca 750
gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800
gtccccagga atccttgtcg catgagctgc cagaacctg gacgtctcaa 850
catcagcacc tgccactgcc actgtcccc tggctacacg ggcagatact 900
gccaagtgcg gtgcagcctg cagtgtgtgc acggccggtt ccgggaggag 950
gagtgctcgt gcgtctgtga catcggctac gggggagccc agtgtgccac 1000
caaggtgcat tttcccttcc acacctgtga cctgaggatc gacgggagact 1050
gcttcatggg gtcttcagag gcagacacct attacagagc caggatgaaa 1100
tgtcagagga aaggcggggg gctggcccag atcaagagcc agaaagtgc 1150

ggacatcctc gccttctatc tgggccgcct ggagaccacc aacgaggtga 1200
 ctgacagtga cttcgagacc aggaacttct ggatcgggct cacctacaag 1250
 accgccaagg actccttccg ctggggccaca ggggagcacc aggccttcac 1300
 cagttttgcc tttgggcagc ctgacaacca cgggctggtg tggctgagtg 1350
 ctgccatggg gtttggcaac tgcgtggagc tgcaggcttc agctgccttc 1400
 aactggaacg accagcgctg caaaaccga aaccgttaca tctgccagtt 1450
 tgcccaggag cacatctccc ggtggggccc agggctctga ggctgacca 1500
 catggctccc tgcctgccc tgggagcacc ggctctgctt acctgtctgc 1550
 ccacctgtct ggaacaaggg ccaggttaag accacatgcc tcatgtccaa 1600
 agaggtctca gacctgcac aatgccagaa gttgggcaga gagaggcagg 1650
 gaggccagtg agggccaggg agtgagtgtt agaagaagct ggggcccttc 1700
 gcctgctttt gattgggaag atgggcttca attagatggc gaaggagagg 1750
 acaccgccag tgggtccaaaa aggctgctct cttccacctg gccagaccc 1800
 tgtggggcag cggagcttcc ctgtggcatg aacccacgg ggtattaaat 1850
 tatgaatcag ctgaaaaaaaa aaaaaa 1876

<210> 50

<211> 455

<212> PRT

<213> Homo Sapien

<400> 50

Met	Leu	His	Pro	Glu	Thr	Ser	Pro	Gly	Arg	Gly	His	Leu	Leu	Ala
1				5					10					15

Val	Leu	Leu	Ala	Leu	Leu	Gly	Thr	Thr	Trp	Ala	Glu	Val	Trp	Pro
			20						25					30

Pro	Gln	Leu	Gln	Glu	Gln	Ala	Pro	Met	Ala	Gly	Ala	Leu	Asn	Arg
			35						40					45

Lys	Glu	Ser	Phe	Leu	Leu	Leu	Ser	Leu	His	Asn	Arg	Leu	Arg	Ser
			50						55					60

Trp	Val	Gln	Pro	Pro	Ala	Ala	Asp	Met	Arg	Arg	Leu	Asp	Trp	Ser
			65						70					75

Asp	Ser	Leu	Ala	Gln	Leu	Ala	Gln	Ala	Arg	Ala	Ala	Leu	Cys	Gly
			80						85					90

Ile	Pro	Thr	Pro	Ser	Leu	Ala	Ser	Gly	Leu	Trp	Arg	Thr	Leu	Gln
			95						100					105

Val	Gly	Trp	Asn	Met	Gln	Leu	Leu	Pro	Ala	Gly	Leu	Ala	Ser	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



09544362-083401

110	115	120
Val Glu Val Val Ser Leu Trp Phe Ala	Glu Gly Gln Arg Tyr Ser	
125	130	135
His Ala Ala Gly Glu Cys Ala Arg Asn	Ala Thr Cys Thr His Tyr	
140	145	150
Thr Gln Leu Val Trp Ala Thr Ser Ser	Gln Leu Gly Cys Gly Arg	
155	160	165
His Leu Cys Ser Ala Gly Gln Thr Ala	Ile Glu Ala Phe Val Cys	
170	175	180
Ala Tyr Ser Pro Gly Gly Asn Trp Glu	Val Asn Gly Lys Thr Ile	
185	190	195
Ile Pro Tyr Lys Lys Gly Ala Trp Cys	Ser Leu Cys Thr Ala Ser	
200	205	210
Val Ser Gly Cys Phe Lys Ala Trp Asp	His Ala Gly Gly Leu Cys	
215	220	225
Glu Val Pro Arg Asn Pro Cys Arg Met	Ser Cys Gln Asn His Gly	
230	235	240
Arg Leu Asn Ile Ser Thr Cys His Cys	His Cys Pro Pro Gly Tyr	
245	250	255
Thr Gly Arg Tyr Cys Gln Val Arg Cys	Ser Leu Gln Cys Val His	
260	265	270
Gly Arg Phe Arg Glu Glu Glu Cys Ser	Cys Val Cys Asp Ile Gly	
275	280	285
Tyr Gly Gly Ala Gln Cys Ala Thr Lys	Val His Phe Pro Phe His	
290	295	300
Thr Cys Asp Leu Arg Ile Asp Gly Asp	Cys Phe Met Val Ser Ser	
305	310	315
Glu Ala Asp Thr Tyr Tyr Arg Ala Arg	Met Lys Cys Gln Arg Lys	
320	325	330
Gly Gly Val Leu Ala Gln Ile Lys Ser	Gln Lys Val Gln Asp Ile	
335	340	345
Leu Ala Phe Tyr Leu Gly Arg Leu Glu	Thr Thr Asn Glu Val Thr	
350	355	360
Asp Ser Asp Phe Glu Thr Arg Asn Phe	Trp Ile Gly Leu Thr Tyr	
365	370	375
Lys Thr Ala Lys Asp Ser Phe Arg Trp	Ala Thr Gly Glu His Gln	
380	385	390
Ala Phe Thr Ser Phe Ala Phe Gly Gln	Pro Asp Asn His Gly Leu	
395	400	405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450

Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
aggaacttct ggatcgggct cacc 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggtggaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaggact ccttcgctg ggccacagg gagcaccagg ccttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
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gtgtccctg tgtgtggggc cgcaggaaga ggcgcagagc tggggccact 150
cttcggagca ggatggactc agggctccga ggcaagtcag actgttcag 200

aggctgaaaa ccaaaccctt gatgacagaa ttctcagtga agtctaccat 250
catttcccgat tatgccttca ctacggtttc ctgcagaatg ctgaacagag 300
cttctgaaga ccaggacatt gagttccaga tgcagattcc agctgcagct 350
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ataaaaccac agaagaaaat ggagagaagg ggactgaaat attcagagct 500
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2331

<210> 55
<211> 694
<212> PRT
<213> Homo Sapien

<400> 55
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20 25 30
Asp Gly Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu
35 40 45
Lys Thr Lys Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile
50 55 60
Ile Ser Arg Tyr Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn
65 70 75
Arg Ala Ser Glu Asp Gln Asp Ile Glu Phe Gln Met Gln Ile Pro
80 85 90
Ala Ala Ala Phe Ile Thr Asn Phe Thr Met Leu Ile Gly Asp Lys
95 100 105
Val Tyr Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp
110 115 120

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu	125	130	135
Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys	140	145	150
Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg	155	160	165
Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln	170	175	180
Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala	185	190	195
Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln	200	205	210
Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser	215	220	225
Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys	230	235	240
Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu	245	250	255
Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile	260	265	270
Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala	275	280	285
Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu	290	295	300
Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys	305	310	315
Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg	320	325	330
Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp	335	340	345
His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val	350	355	360
Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly	365	370	375
Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His	380	385	390
Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr	395	400	405
Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu			

410	415	420
Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr		
425	430	435
Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu		
440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu		
455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr		
470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val		
485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser		
500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His		
515	520	525
Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile		
530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp		
545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr		
560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu		
575	580	585
Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg		
590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu		
605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met		
620	625	630
Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro		
635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly		
650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys		
665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His		
680	685	690
Leu Gly Ile Arg		

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactccggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgctcct tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaggacc acttgatata agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
cggacgcgtg ggggtgccga catggcgagt gtagtgctgc cgagcggatc 50
ccagtgtgag gcggcagcgg cggcggcggc gcctcccggg ctccggcttc 100
tgctgttget cttctccgcc ggggcaactga tccccacagg tgatgggcag 150
aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgaccat 200

cagttgccaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250
ccaacaggca gaccatttat ttcagggact tcaggccttt gaaggacagc 300
aggtttcagt tgctgaatth ttctagcagt gaactcaaag tatcattgac 350
aaacgtotca attttctgatg aaggaagata cttttgccag ctctataaccg 400
atccccca ggaagttac accaccatca cagtcctggg cccaccacgt 450
aatctgatga togatataca gaaagacact gcgggtggaag gtgaggagat 500
tgaagtaac tgcactgcta tggccagcaa gccagccacg actatcaggt 550
ggttcaaagg gaacacagag ctaaaaggca aatcggaggt ggaagagtgg 600
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ggacgatggg gtcccagtga tctgccaggt ggagcaccct gcggtcactg 700
gaaacctgca gaccacgagg tatctagaag tacagtataa gcctcaagtg 750
cacattcaga tgacttatcc tctacaaggc ttaaccgggg aaggggacgc 800
gcttgagtta acatgtgaag ccatcgggaa gccccagcct gtgatggtaa 850
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cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataaccg 950
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gaggacagaa caactccgaa gaaaagaaag agtacttcat ctagatcagc 1350
ctttttgttt caatgaggtg tccaactggc cctattttaga tgataaagag 1400
acagtgatat tgg 1413

<210> 61

<211> 440

<212> PRT

<213> Homo Sapien

<400> 61

Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala
1 5 10 15

00944566-0033404

Ala	Ala	Ala	Ala	Ala	Pro	Pro	Gly	Leu	Arg	Leu	Leu	Leu	Leu	Leu	Leu	20	25	30
Phe	Ser	Ala	Ala	Ala	Leu	Ile	Pro	Thr	Gly	Asp	Gly	Gln	Asn	Leu		35	40	45
Phe	Thr	Lys	Asp	Val	Thr	Val	Ile	Glu	Gly	Glu	Val	Ala	Thr	Ile		50	55	60
Ser	Cys	Gln	Val	Asn	Lys	Ser	Asp	Asp	Ser	Val	Ile	Gln	Leu	Leu		65	70	75
Asn	Pro	Asn	Arg	Gln	Thr	Ile	Tyr	Phe	Arg	Asp	Phe	Arg	Pro	Leu		80	85	90
Lys	Asp	Ser	Arg	Phe	Gln	Leu	Leu	Asn	Phe	Ser	Ser	Ser	Glu	Leu		95	100	105
Lys	Val	Ser	Leu	Thr	Asn	Val	Ser	Ile	Ser	Asp	Glu	Gly	Arg	Tyr		110	115	120
Phe	Cys	Gln	Leu	Tyr	Thr	Asp	Pro	Pro	Gln	Glu	Ser	Tyr	Thr	Thr		125	130	135
Ile	Thr	Val	Leu	Val	Pro	Pro	Arg	Asn	Leu	Met	Ile	Asp	Ile	Gln		140	145	150
Lys	Asp	Thr	Ala	Val	Glu	Gly	Glu	Glu	Ile	Glu	Val	Asn	Cys	Thr		155	160	165
Ala	Met	Ala	Ser	Lys	Pro	Ala	Thr	Thr	Ile	Arg	Trp	Phe	Lys	Gly		170	175	180
Asn	Thr	Glu	Leu	Lys	Gly	Lys	Ser	Glu	Val	Glu	Glu	Trp	Ser	Asp		185	190	195
Met	Tyr	Thr	Val	Thr	Ser	Gln	Leu	Met	Leu	Lys	Val	His	Lys	Glu		200	205	210
Asp	Asp	Gly	Val	Pro	Val	Ile	Cys	Gln	Val	Glu	His	Pro	Ala	Val		215	220	225
Thr	Gly	Asn	Leu	Gln	Thr	Gln	Arg	Tyr	Leu	Glu	Val	Gln	Tyr	Lys		230	235	240
Pro	Gln	Val	His	Ile	Gln	Met	Thr	Tyr	Pro	Leu	Gln	Gly	Leu	Thr		245	250	255
Arg	Glu	Gly	Asp	Ala	Leu	Glu	Leu	Thr	Cys	Glu	Ala	Ile	Gly	Lys		260	265	270
Pro	Gln	Pro	Val	Met	Val	Thr	Trp	Val	Arg	Val	Asp	Asp	Glu	Met		275	280	285
Pro	Gln	His	Ala	Val	Leu	Ser	Gly	Pro	Asn	Leu	Phe	Ile	Asn	Asn		290	295	300
Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn				

305	310	315
Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp		
320	325	330
Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr		
335	340	345
Thr Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg		
350	355	360
Ala Gly Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile		
365	370	375
Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu		
380	385	390
Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe		
395	400	405
Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr		
410	415	420
Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser Glu Glu Lys		
425	430	435
Lys Glu Tyr Phe Ile		
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- <210> 62
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 62
- ggctttctgct gttgctcttc tccg 24
- <210> 63
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 63
- gtacactgtg accagtcagc 20
- <210> 64
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
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ggctccctgc gcgcgcgcg cctcccggga cagaagatgt gctccagggt 150
ccctctgtg ctgcgcgtgc tctgtctact ggccctgggg cctgggggtgc 200
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ttgccggcct gccgggcctg cagctcctgg acctgtcaca gaaccagatc 400



094456-03404

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 atttattctg ggaagatgtt tttcaaactc agagacaagg actttggttt 2500
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 aaaaa 2555

<210> 69
 <211> 598
 <212> PRT
 <213> Homo Sapien

<400> 69
 Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu Leu
 1 5 10 15
 Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys
 20 25 30
 Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
 35 40 45
 Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
 50 55 60
 Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu
 65 70 75
 Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
 80 85 90
 Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser
 95 100 105
 Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

				110					115					120
Ala	Leu	Arg	Leu	Ala	Gly	Leu	Gly	Leu	Gln	Gln	Leu	Asp	Glu	Gly
				125					130					135
Leu	Phe	Ser	Arg	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp
				140					145					150
Asn	Gln	Leu	Glu	Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly
				155					160					165
Leu	Thr	Arg	Leu	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu
				170					175					180
Arg	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp
				185					190					195
Val	Ser	Asn	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly
				200					205					210
Leu	Phe	Pro	Arg	Leu	Arg	Leu	Leu	Ala	Ala	Ala	Arg	Asn	Pro	Phe
				215					220					225
Asn	Cys	Val	Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu
				230					235					240
Ser	His	Val	Thr	Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe
				245					250					255
Pro	Pro	Lys	Asn	Ala	Gly	Arg	Leu	Leu	Leu	Glu	Leu	Asp	Tyr	Ala
				260					265					270
Asp	Phe	Gly	Cys	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr
				275					280					285
Thr	Arg	Pro	Val	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	Ser	Leu
				290					295					300
Ala	Pro	Thr	Trp	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Thr	Glu	Ala	Pro
				305					310					315
Ser	Pro	Pro	Ser	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln
				320					325					330
Pro	Gln	Asp	Cys	Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys
				335					340					345
His	Leu	Gly	Thr	Arg	His	His	Leu	Ala	Cys	Leu	Cys	Pro	Glu	Gly
				350					355					360
Phe	Thr	Gly	Leu	Tyr	Cys	Glu	Ser	Gln	Met	Gly	Gln	Gly	Thr	Arg
				365					370					375
Pro	Ser	Pro	Thr	Pro	Val	Thr	Pro	Arg	Pro	Pro	Arg	Ser	Leu	Thr
				380					385					390
Leu	Gly	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Gly	Leu
				395					400					405

004460-0340

Gln Arg Tyr Leu	Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410	415	420
Leu Thr Tyr Arg	Asn Leu Ser Gly Pro	Asp Lys Arg Leu Val Thr
425	430	435
Leu Arg Leu Pro	Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu	
440	445	450
Arg Pro Asn Ala	Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro	
455	460	465
Gly Arg Val Pro	Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr	
470	475	480
Pro Pro Ala Val	His Ser Asn His Ala Pro Val Thr Gln Ala Arg	
485	490	495
Glu Gly Asn Leu	Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val	
500	505	510
Leu Leu Ala Ala	Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg	
515	520	525
Arg Gly Arg Ala	Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val	
530	535	540
Gly Pro Gly Ala	Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro	
545	550	555
Leu Glu Pro Gly	Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu	
560	565	570
Pro Ser Gly Ser	Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly	
575	580	585
Pro Gly Leu Gln	Ser Pro Leu His Ala Lys Pro Tyr Ile	
590	595	

<210> 70

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ccctccactg ccccaccgac tg 22

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

ctgcccacg tccacctgcc tcaat 25

<210> 73

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 73

aggactgcc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 74

acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75

<211> 1077

<212> DNA

<213> Homo Sapien

<400> 75

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cgccccgcca cctccttget accccactct tgaaaccaca gctgttggca 100

gggtccccag ctcatgccag cctcatctcc tttcttgcta gccccaaag 150

ggcctccagg caacatgggg ggcccagtca gagagccggc actctcagtt 200

gccctctggt tgagttgggg ggcagctctg ggggcccgtg cttgtgccat 250

ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300

gccggctgca ggggacagga ggccccccc agaatgggga agggatatccc 350

tggcagagtc tcccggagca gagttccgat gccctggaag cctgggagaa 400

tggggagaga tccccgaaaa ggagagcagt gctcacccaa aaacagaaga 450
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 ccaggggtggg tacatactgg agacagccaa gagctgagta tataaaggag 950
 agggaatgtg caggaacaga ggcactctcc tgggtttggc tccccgttcc 1000
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 cttgcttctg ttccccatgg agctccg 1077

<210> 76
 <211> 250
 <212> PRT
 <213> Homo Sapien

<400> 76
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
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 Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
 20 25 30
 Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
 35 40 45
 Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
 50 55 60
 Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
 65 70 75
 Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
 80 85 90
 Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
 95 100 105
 Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
 110 115 120

Val	Pro	Ile	Asn	Ala	Thr	Ser	Lys	Asp	Asp	Ser	Asp	Val	Thr	Glu
				125					130					135
Val	Met	Trp	Gln	Pro	Ala	Leu	Arg	Arg	Gly	Arg	Gly	Leu	Gln	Ala
				140					145					150
Gln	Gly	Tyr	Gly	Val	Arg	Ile	Gln	Asp	Ala	Gly	Val	Tyr	Leu	Leu
				155					160					165
Tyr	Ser	Gln	Val	Leu	Phe	Gln	Asp	Val	Thr	Phe	Thr	Met	Gly	Gln
				170					175					180
Val	Val	Ser	Arg	Glu	Gly	Gln	Gly	Arg	Gln	Glu	Thr	Leu	Phe	Arg
				185					190					195
Cys	Ile	Arg	Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	Tyr	Asn	Ser
				200					205					210
Cys	Tyr	Ser	Ala	Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	Ile	Leu
				215					220					225
Ser	Val	Ile	Ile	Pro	Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro
				230					235					240
His	Gly	Thr	Phe	Leu	Gly	Phe	Val	Lys	Leu					
				245					250					

<210> 77
 <211> 2849
 <212> DNA
 <213> Homo Sapien

<400> 77
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 gggggggacc tgtggctgct cgtaccgcc cccaccctcc tcttctgcac 150
 tgccgtcttc cggaagacct tttcccttgc tctgtttctc tcaccgagtc 200
 tgtgcacgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250
 ctctaggggc ggcgcgggag gagcgcccg cgggacggag ggcccggcag 300
 gaagatgggc tccctgggac agggactctt gctggcgtag tgccctgctc 350
 ttgcctttgc ctctggcctg gtctgagtc gtgtgcccc tgtccagggg 400
 gaacagcagg agtgggaggg gactgaggag ctgccgtcgc ctccggacca 450
 tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500
 aggggtctcc tgcctcccg tgccttgcgt gctgtgacct cggtaacctc 550
 atgtaccgag cgaccgcgt gcccagatc aacatcacta tcttgaaagg 600
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<210> 78

<211> 281

<212> PRT

<213> Homo Sapien

<400> 78

Met Gly Ser Arg Gly Gln Gly Leu Leu Leu Ala Tyr Cys Leu Leu
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Leu Ala Phe Ala Ser Gly Leu Val Leu Ser Arg Val Pro His Val
 20 25 30

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
 35 40 45

Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
 50 55 60

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
 65 70 75

Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
 80 85 90

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
 95 100 105

Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

110	115	120
Ala Arg Gly His Thr Gly Pro Lys Gly	Gln Lys Gly Ser Met Gly	
125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His	Tyr Ala Ala Phe Ser Val	
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn	His Tyr Tyr Gln Thr Val	
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu	Tyr Asp His Phe Asn Met	
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val	Pro Gly Leu Tyr Phe Phe	
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln	Lys Glu Thr Tyr Leu His	
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val	Ile Leu Phe Ala Gln Val	
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln	Ser Leu Met Leu Glu Leu	
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg	Leu Tyr Lys Gly Glu Arg	
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu	Asp Thr Tyr Ile Thr Phe	
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr	Glu Pro	
275	280	

<210> 79

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 79

tacaggccca gtcaggacca gggg 24

<210> 80

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 80

ctgaagaagt agaggccggg cacg 24

<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccgtgctt ggcgtgctgt gaccccggtta cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 82
gaggagcatc cgctgcggtc ctgcgcgaga ccccgcgcg gattcgccgg 50
tccttccgc gggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100
ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150
cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200
gacaaaaact aaactgaaat ttaaaatgtt cttcggggga gaaggagct 250
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agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350
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cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050

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tatgcaaaga aacagggttag gacatctagg ttccaattca ttcacattct 2150
tggttccaga taaaatcaac tgtttatata aatttctaata ggatttgctt 2200
ttctttttat atggattcct ttaaaaactta ttccagatgt agttccttcc 2250
aattaaatat ttgaataaat cttttgttac tcaa 2284

<210> 83
<211> 431
<212> PRT
<213> Homo Sapien

<400> 83
Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile
1 5 10 15

004433-0010

Ile Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu	20	25	30
Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu	35	40	45
Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln	50	55	60
Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly	65	70	75
Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala	80	85	90
Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala	95	100	105
Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile	110	115	120
Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu	125	130	135
Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val	140	145	150
Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp	155	160	165
Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp	170	175	180
His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu	185	190	195
Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser	200	205	210
Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala	215	220	225
Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala	230	235	240
Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr	245	250	255
Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro	260	265	270
Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr	275	280	285
Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr	290	295	300
Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly			

305	310	315
Ser Leu Glu Thr Ile Pro Phe Thr Glu	Ile Ser Asn Leu Thr Leu	
320	325	330
Asn Thr Gly Asn Val Tyr Asn Pro Thr	Ala Leu Ser Met Ser Asn	
335	340	345
Val Glu Ser Ser Thr Met Asn Lys Thr	Ala Ser Trp Glu Gly Arg	
350	355	360
Glu Ala Ser Pro Gly Ser Ser Ser Gln	Gly Ser Val Pro Glu Asn	
365	370	375
Gln Tyr Gly Leu Pro Phe Glu Lys Trp	Leu Leu Ile Gly Ser Leu	
380	385	390
Leu Phe Gly Val Leu Phe Leu Val Ile	Gly Leu Val Leu Leu Gly	
395	400	405
Arg Ile Leu Ser Glu Ser Leu Arg Arg	Lys Arg Tyr Ser Arg Leu	
410	415	420
Asp Tyr Leu Ile Asn Gly Ile Tyr Val	Asp Ile	
425	430	

<210> 84
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 84
 agggaggatt atccttgacc tttgaagacc 30

 <210> 85
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 85
 gaagcaagtg cccagctc 18

 <210> 86
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 86
 cgggtccctg ctctttgg 18

<210> 87
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
cacccgtagct gggagcgcac tcac 24

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
agtgttaagtc aagctccc 18

<210> 89
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[illegible]

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 Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
 185 190 195
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 200 205 210
 Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
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 Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
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